# 3dDeconvolve

## Advanced Features

**Just in case you weren't confused enough already**

# Other Features of 3dDeconvolve - 1

- **`-input1D`** = used to process a single time series, rather than a dataset full of time series
  - ⋆ e.g., test out a stimulus timing sequence on sample data
  - ⋆ **`-nodata`** option can be used to check for collinearity
- **`-censor`** = used to turn off processing for some time points
  - ⋆ for time points that are "bad" (e.g., too much movement; scanner hiccup)
  - ⋆ **`-CENSORTR 2:37`** = newer way to specify omissions (e.g., run #2, index #37)
- **`-sresp`** = output standard deviation of HRF ($\beta$) estimates
  - ⋆ can then plot error bands around HRF in AFNI graph viewer
- **`-errts`** = output residuals (difference between fitted model and data)
  - ⋆ for statistical analysis of time series noise
- **`-TR_times dt`** = calculate **`-iresp`** and **`-sresp`** HRF results with time step **`dt`** (instead of input dataset TR)
  - ⋆ Can be used to make HRF graphs look better
- **`-jobs`** ***N*** = run with independent threads — ***N*** of them
  - ⋆ extra speed, if you have a dual-CPU system (or more)!

# Other Features - 2

**http://afni.nimh.nih.gov/pub/dist/doc/misc/Decon/DeconSummer2004.html**
**http://afni.nimh.nih.gov/pub/dist/doc/misc/Decon/DeconSpring2007.html**

- Equation solver: Program computes **condition number** for **X** matrix (measures of how sensitive regression results are to changes in **X**)
  - ★ If the condition number is "bad" (too big), then the program will not actually proceed to compute the results
  - ★ You can use the **-GOFORIT** option on the command line to force the program to run despite **X** matrix warnings
    - o But you should strive to understand why you are getting these warnings!!
- Other matrix checks:
  - ★ Duplicate stimulus filenames, duplicate regression matrix columns, all zero matrix columns
- Check the screen output for **WARNING**s and **ERROR**s
  - ★ Such messages also saved into file **3dDeconvolve.err**

# Other Features - 3

- All-zero regressors *are* allowed (via `-allzero_OK` or `-GOFORIT`)
  - ★ Will get zero weight in the solution
  - ★ Example: task where subject makes a choice for each stimulus (e.g., male or female face?)
    - o You want to analyze correct and incorrect trials as separate cases
    - o What if some subject makes no mistakes? Hmmm…
      - ➥ Can keep the all-zero regressor (e.g., all `-stim_times` = `*`)
      - ➥ Input files and output datasets for error-making and perfect-performing subjects will be organized the same way

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- `3dDeconvolve_f` program can be used to compute linear regression results in single precision (7 decimal places) rather than double precision (16 places)
  - ★ For better speed, but with lower numerical accuracy
  - ★ Best to do at least one run ***both*** ways to check if results differ significantly (Equation solver *should* be safe, but …)

# Other Features - 4

- Default output format is 16-bit short integers, with a scaling factor for each sub-brick to convert it to floating point values
  - ★ `-float` option can be used to get 32-bit floating point format output — more precision, and more disk space

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- `3dDeconvolve` recommends a `-polort` value, and prints that out as well as the value you chose (or defaulted to)
  - ★ `-polort A` can be used to let the program set the detrending (AKA "high pass filtering", since detrending removes low frequency content from data) level automatically

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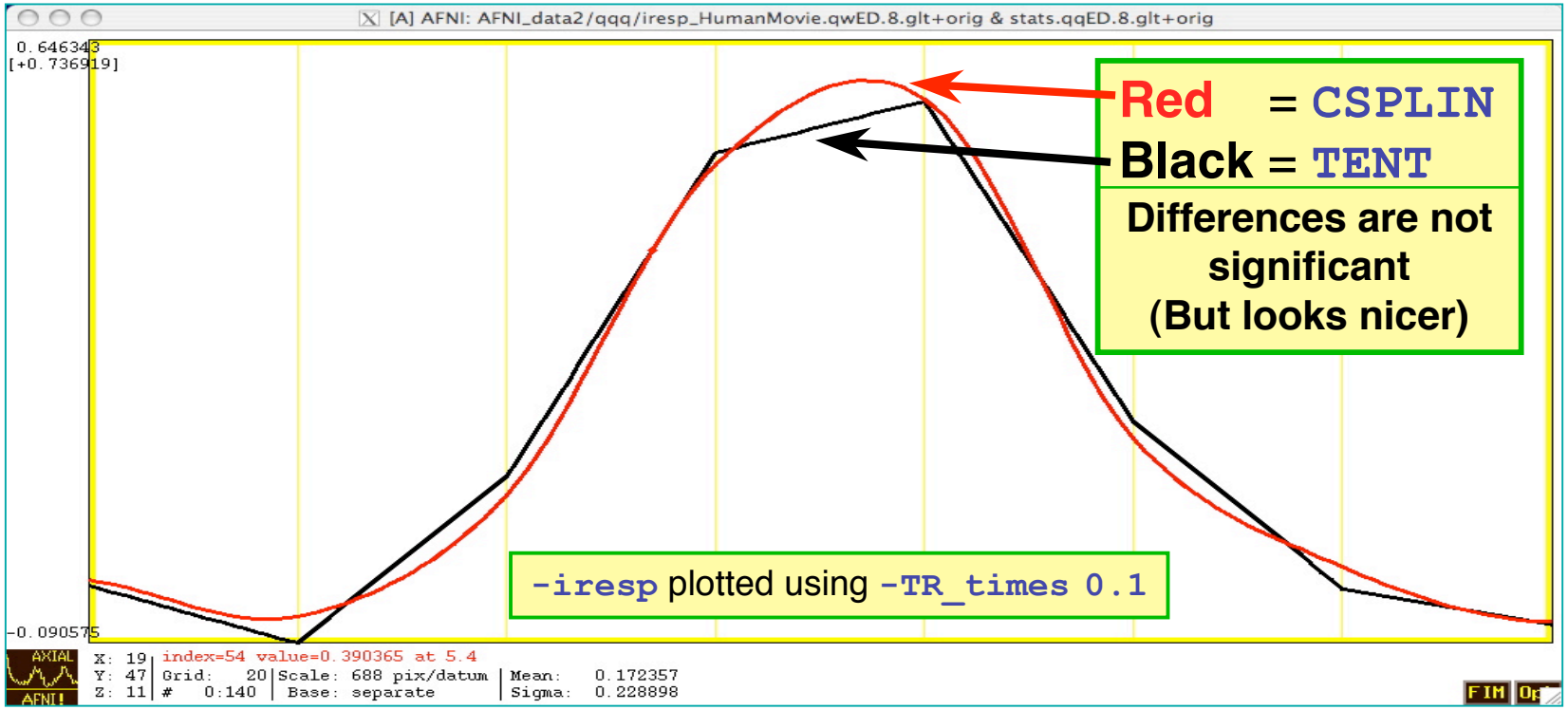
- `-stim_file` is used to input a column directly into **X** matrix
  - ★ Motion parameters (as in previous examples)
  - ★ If you create a stimulus+response model outside `3dDeconvolve` (e.g., using program `waver`)

# Other Features - 5

- `-stim_times` has some other basis function options for the HRF model besides **`BLOCK`** and **`TENT`**
  - ★ **`CSPLIN`** = cubic spline instead of **`TENT`** = linear spline
    - o Same parameters: `(start,stop,number of regressors)`
    - o Can be used as a “drop in” replacement for **`TENT`**



# Other Features - 6

- `-fitts` option is used to create a synthetic dataset
  - ★ each voxel time series is full (signal+baseline) model as fitted to the data time series in the corresponding voxel location

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- `3dSynthesize` program can be used to create synthetic datasets from *subsets* of the full model
  - ★ Uses `-x1D` and `-cbucket` outputs from `3dDeconvolve`
    - o `-cbucket` stores $\beta$ coefficients for each $\mathbf{X}$ matrix column into dataset
    - o `-x1D` stores the matrix columns (and `-stim_label`s)
  - ★ Potential uses:
    - o Baseline only dataset
      - ➥ `3dSynthesize -cbucket fred+orig -matrix fred.x1D -select baseline -prefix fred_base`
      - ➥ Could subtract this dataset from original data (via `3dcalc`) to get signal+noise dataset that has no baseline component left
    - o Just one stimulus class model (+ baseline) dataset
      - ➥ `3dSynthesize -cbucket fred+orig -matrix fred.x1D -select baseline Faces -prefix fred_Faces`

# Other Recent Small Changes

- Defaults are changed:
  - ★ `-nobout` & `-full_first` & `-bucket` & `-x1D` are always implied
  - ★ Names of statistics sub-bricks are slightly altered (to be more consistent)

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- Checks if `-stim_times` inputs are out of range (AKA: the PSFB syndrome)
  - ★ Prints `WARNING` message, but continues analysis

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- When using `-nodata` with `-stim_times`, it is important to give the number of time points and the TR, as in `-nodata 250 2.3`
  - ★ With `-input1D`, use `-TR_1D 2.3` to specify TR

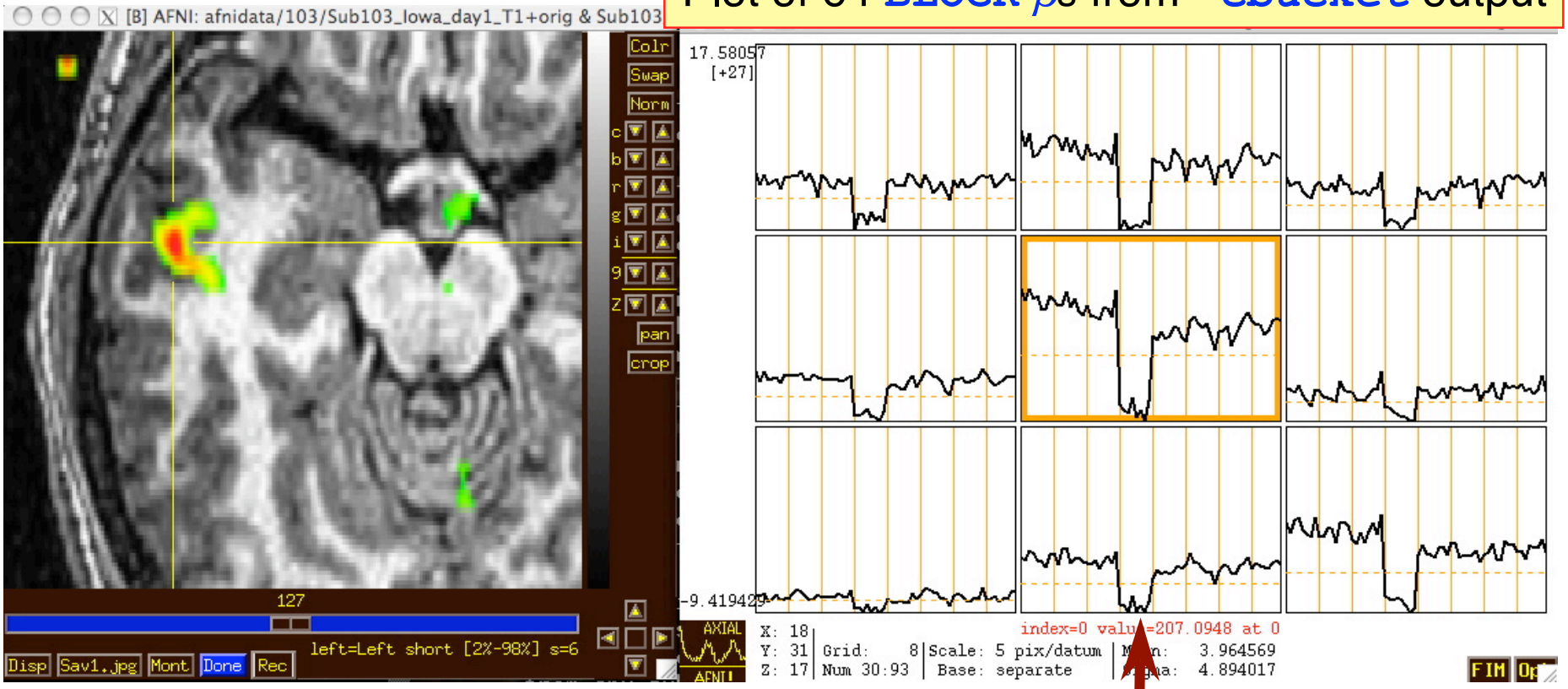
# IM Regression - 1

- **IM** = **I**ndividual **M**odulation
  - ★ Compute separate amplitude of response for each stimulus
    - o Instead of computing average amplitude of responses to multiple stimuli in the same class
  - ★ Response amplitudes ($\beta$s) for each individual block/event will be highly noisy
    - o Can't use individual activation map for much
    - o Must pool the computed $\beta$s in some further statistical analysis (e.g., a *t*-test via `3dttest`?)
  - ★ Usage: **`-stim_times_IM k tname model`**
    - o Like **`-stim_times`**, but creates a separate regression matrix column for each time given

# IM Regression - 2

- Only application of IM thus far has been in checking some data we received from another institution
- Experiment: 64 blocks of sensorimotor task (8 runs each with 8 blocks)

Plot of 64 **BLOCK** $\beta$s from **-cbucket** output




N.B.: sign reversal in run #4 = stimulus timing error!

# IM Regression - 3

- IM works naturally with blocks, which only have 1 amplitude parameter per stimulus
- With event-related experiment and deconvolution, have multiple amplitude parameters per stimulus
  - ★ Difficulty: each event in same class won't get the same shaped HRF this way
  - ★ Desideratum: allow response shape to vary (that's deconvolution), but only allow amplitude to vary between responses in the same stimulus class
  - ★ Problem: get unknowns that multiply each other (shape parameters × amplitude parameters) — and we step outside the realm of ***linear*** analysis
  - ★ Possible solution: **Total Least Squares** mathematical methodology — am investigating now

# AM Regression - 1

- **AM** = **A**mplitude **M**odulated (or Modulation)
  - ★ Have some extra data measured about each response to a stimulus, and *maybe* the BOLD response amplitude is modulated by this
  - ★ Reaction time; Galvanic skin response; Pain level perception; Emotional valence (happy or sad or angry face?)
- Want to see if some brain activations vary proportionally to this **ABI** (**A**uxiliary **B**ehaviorial **I**nformation)

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- Discrete levels (2 or maybe 3) of ABI:
  - ★ Separate the stimuli into sub-classes that are determined by the ABI ("on" and "off", maybe?)
  - ★ Use a GLT to test if there is a difference between the FMRI responses in the sub-classes

```
3dDeconvolve ...                                                    \
 -stim_times 1 regressor_on.1D  'BLOCK(2,1)' -stim_label 1 'On'   \
 -stim_times 2 regressor_off.1D 'BLOCK(2,1)' -stim_label 2 'Off' \
 -gltsym 'SYM: +On | +Off' -glt_label 1 'On+Off'                   \
 -gltsym 'SYM: +On -Off'   -glt_label 2 'On-Off' ...
```

  - "`On+Off`" tests for any activation in *either* the "on" or "off" conditions
  - "`On-Off`" tests for differences in activation *between* "on" and "off" conditions
  - Can use `3dcalc` to threshold on ***both*** statistics at once to find a **conjunction**

# AM Regression - 2

- Continuous (or several finely graded) ABI levels
  - ★ Want to find active voxels whose activation level also depends on ABI
  - ★ `3dDeconvolve` is a linear program, so must make the assumption that the change in FMRI signal as ABI changes is linearly proportional to the changes in the ABI values
- Need to make 2 separate regressors
  - ★ One to find the mean FMRI response (the usual `-stim_times` analysis)
  - ★ One to find the variations in the FMRI response as the ABI data varies
- The second regressor should have the form

$$r_{\mathrm{AM2}}(t) = \sum_{k=1}^{K} h(t-\tau_k)\cdot(a_k - \bar{a})$$

  - ★ Where $a_k$ = value of $k^{\mathrm{th}}$ ABI value, and $\bar{a}$ is the average ABI value
- Response ($\beta$) for first regressor is standard activation map
- Statistics and $\beta$ for second regressor make activation map of places whose BOLD response changes with changes in ABI
  - ★ Using 2 regressors allows separation of voxels that are active but are *not* detectably modulated by the ABI from voxels that *are* ABI-sensitive

# AM Regression - 3

- New feature of **3dDeconvolve**: **-stim_times_AM2**
- Use is very similar to standard **-stim_times**
  - ★ **-stim_times_AM2 1 times_ABI.1D 'BLOCK(2,1)'**
  - ★ The **times_ABI.1D** file has time entries that are "married" to ABI values:

```
10*5 23*4 27*2 39*5
17*2 32*5
*
16*2 24*3 37*5 41*4
```

  - ★ Such files can be created from 2 standard ASCII .1D files using the new **1dMarry** program
    - o The **-divorce** option can be used to split them up
- **3dDeconvolve** automatically creates the two regressors (unmodulated and amplitude modulated)
  - ★ Use **-fout** option to get statistics for activation of the pair of regressors (i.e., testing null hypothesis that *both* $\beta$ weights are zero: that there is no ABI-independent *or* ABI-proportional signal change)
  - ★ Use **-tout** option to test each $\beta$ weight separately
  - ★ Can **1dplot** $\mathbf{X}$ matrix columns to see each regressor

# AM Regression - 4

- The **AM** feature is new, and so needs some practical user experiences before it can be considered "standard practice"
  - ★ In particular: don't know how much data or how many events are needed to get good ABI-dependent statistics
- If you want, **`-stim_times_AM1`** is also available
  - ★ It only builds the regressor proportional to ABI data directly, with no mean removed:

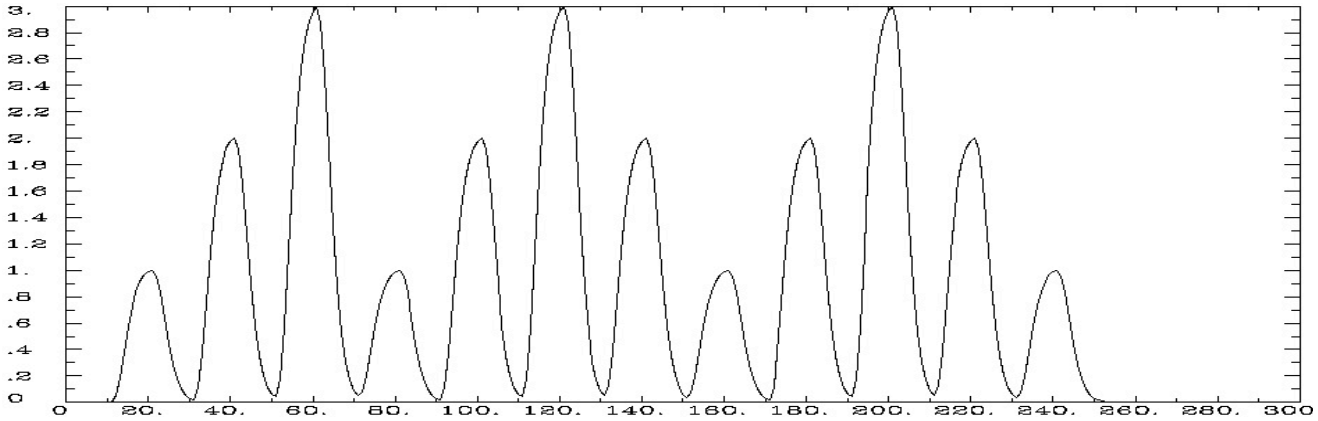
$$r_{\mathrm{AM1}}(t) = \sum_{k=1}^{K} h(t-\tau_k)\cdot a_k$$

  - ★ Can't imagine what value this option has, but you never know … (if you can think of a good use, let me know)
- Future directions:
  - ★ Allow more than one amplitude to be married to each stimulus time (insert obligatory polygamy/polyandry joke here)
    - o How many ABI types at once is too many? I don't know.
  - ★ How to deal with unknown nonlinearities in the BOLD response to ABI values? I don't know. (Regress each event separately, then compute MI?)
  - ★ Deconvolution with amplitude modulation? Requires more thought.

# AM Regression - 5

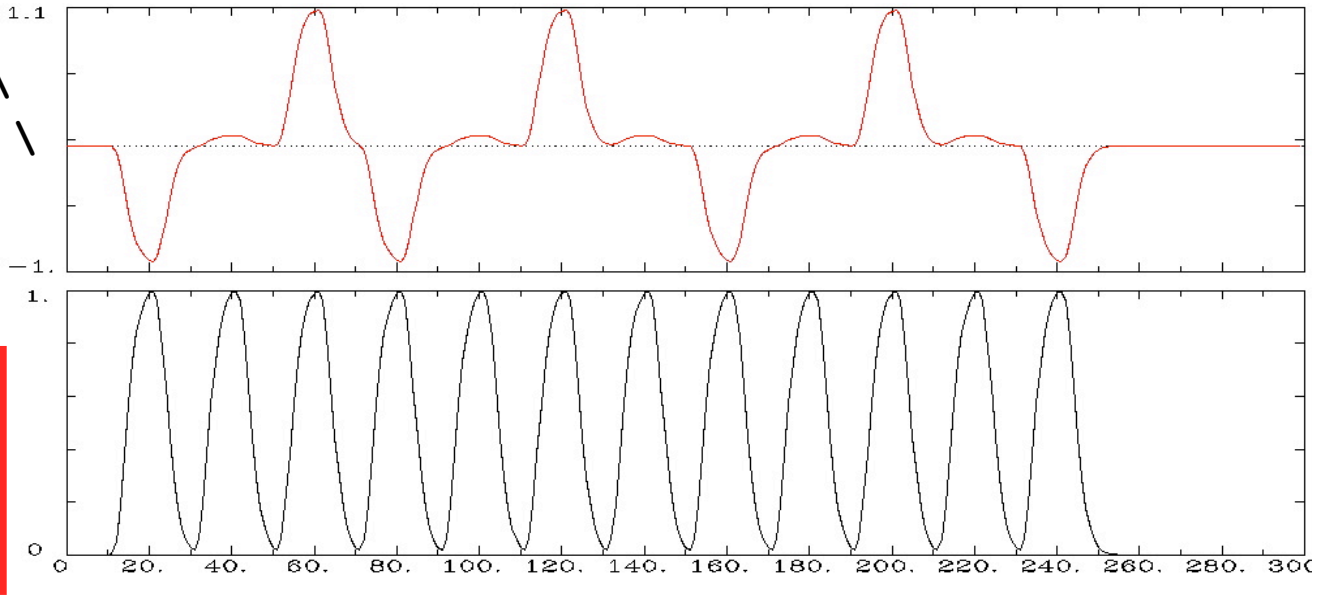
Timing: **AM.1D** = `10*1 30*2 50*3 70*1 90*2 110*3 130*2 150*1 170*2 190*3 210*2 230*1`

- `3dDeconvolve -nodata 300 1.0 -num_stimts 1 \`
  `-stim_times_AM1 1 AM.1D 'BLOCK(10,1)' -x1D AM1.x1D`
- `1dplot AM1.x1D'[2]'`




**AM1** model of signal (modulation = ABI)

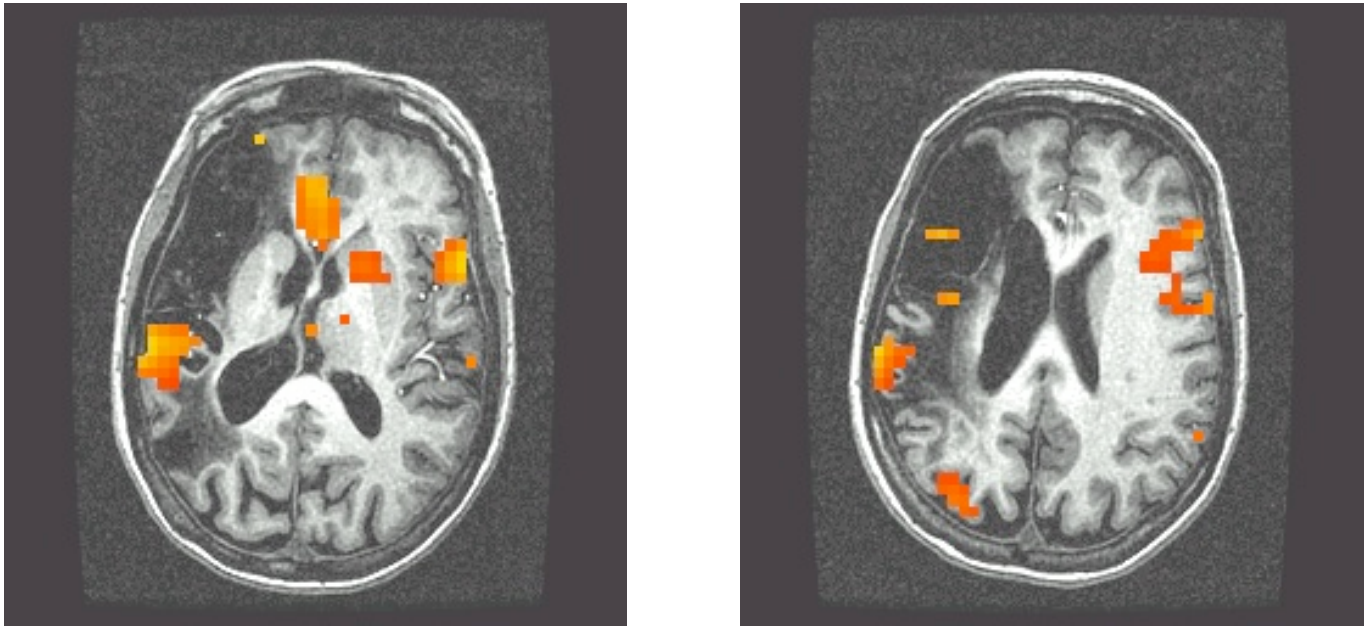
- `3dDeconvolve -nodata 300 1.0 \`
  `-num_stimts 1 \`
  `-stim_times_AM2 1 \`
  `AM.1D 'BLOCK(10,1)' \`
  `-x1D AM2.x1D`
- `1dplot -sepscl \`
  `AM2.x1D'[2,3]'`




**AM2** model of signal: is 2D sub-space spanned by these 2 time series

# AM Regression - 6

- First actual user: Whitney Postman (formerly NIDCD; PI=Al Braun)
- Picture naming task in aphasic stroke patient
- ABI data = number of alternative names for each image (e.g., "balcony" & "porch" & "veranda", vs. "strawberry"), from 1 to 18
  - 8 imaging runs, 144 stimulus events
- 2 slices showing activation map for BOLD responses proportional to ABI ($\beta_{AM2}$)
  - What does this mean? Don't ask me!

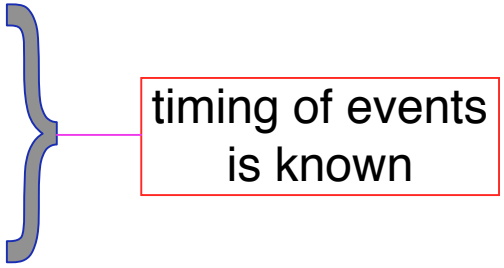


# AM Regression - 7

- Alternative: use **IM** to get individual $\beta$s for each block/event and then do external regression statistics on those values
- Could do nonlinear fitting via `3dNLfim`, or inter-class contrasts via `3dttest`, `3dLME`, `3dANOVA`, etc.
- What is better: **AM** or **IM+** ?
  - We don't know – experience with these options is limited thus far – you can always try both!
  - If **AM** doesn't fit your models/ideas, then **IM** is clearly the way to go
  - Probably need to consult with SSCC to get some hints/advice

# Other Advanced Topics in Regression

- Can have activations with multiple phases that are not always in the same time relationship to each other; e.g.:
  a) subject gets cue #1
  b) variable waiting time ("hold")
  c) subject gets cue #2, emits response
     ➥ which depends on both cue #1 and #2



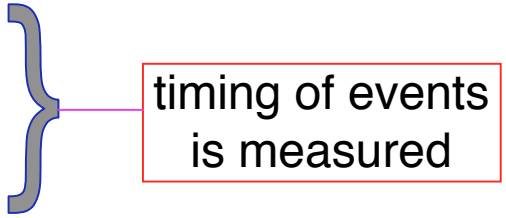

★ Cannot treat this as one event with one HRF, since the different waiting times will result in different overlaps in separate responses from cue #1 and cue #2

★ Solution is multiple HRFs: separate HRF (fixed shape or deconvolution) for cue #1 times and for cue #2 times

- Must have significant variability in inter-cue waiting times, or will get a nearly-collinear model
  ➥ impossible to tell tail end of HRF #1 from the start of HRF #2, if always locked together in same temporal relationship
- How much variability is "significant"? Good question.

# Even More Complicated Case

- Solving a visually presented puzzle:
  a) subject sees puzzle
  b) subject cogitates a while
  c) subject responds with solution




- The problem is that we expect some voxels to be significant in phase (b) as well as phases (a) and/or (c)
- Variable length of phase (b) means that shape for its response varies between trials
  - ★ Which is contrary to the whole idea of averaging trials together to get decent statistics (which is basically what linear regression for the $\beta$ weights does, in an elaborate sort of way)
- Could assume response ***amplitude*** in phase (b) is constant across trials, and response ***duration*** varies directly with time between phases (a) and (c)
  - ★ Need three HRFs
  - ★ Can't generate (b) HRF in `3dDeconvolve`

# Noise Issues

- "Noise" in FMRI is caused by several factors, not completely characterized
  - ★ MR thermal noise (well understood, unremovable)
  - ★ Cardiac and respiratory cycles (partly understood)
    - o In principle, could measure these sources of noise separately and then try to regress them out
      - ➥ RETROICOR program underway (Rasmus Birn of FIM/NIMH)
  - ★ Scanner fluctuations (e.g., thermal drift of hardware)
  - ★ Small subject head movements (10-100 mm)
  - ★ Very low frequency fluctuations (periods longer than 100 s)
- Data analysis should try to remove what can be removed and allow for the statistical effects of what can't be removed
  - ★ "Serial correlation" in the noise time series affects the *t*- and *F*-statistics calculated by `3dDeconvolve`
  - ★ At present, nothing is done to correct for this effect (by us)

# Nonlinear Regression

- Linear models aren't the only possibility
  - ★ e.g., could try to fit HRF of the form $h(t) = a \cdot t^b \cdot e^{-t/c}$
  - ★ Unknowns $b$ and $c$ appear nonlinearly in this formula
- Program **3dNLfim** can do nonlinear regression (including nonlinear deconvolution)
  - ★ User must provide a C function that computes the model time series, given a set of parameters (e.g., $a$, $b$, $c$)
    - o We could help you develop this C model function
    - o Several sample model functions in the AFNI source code distribution
  - ★ Program then drives this C function repeatedly, searching for the set of parameters that best fit each voxel
  - ★ Has been used to fit pharmacological wash-in/wash-out models (difference of two exponentials) to FMRI data acquired during pharmacological challenges
    - o e.g., injection of nicotine, cocaine, ethanol, etc.
    - o these are difficult experiments to do ***and*** to analyze

# Spatial Models of Activation

- Smooth data in space before analysis

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- Average data across anatomically-selected regions of interest ROI (before or after analysis)
  - Labor intensive (*i.e.*, hire more students)

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- Reject isolated small clusters of above-threshold voxels after analysis

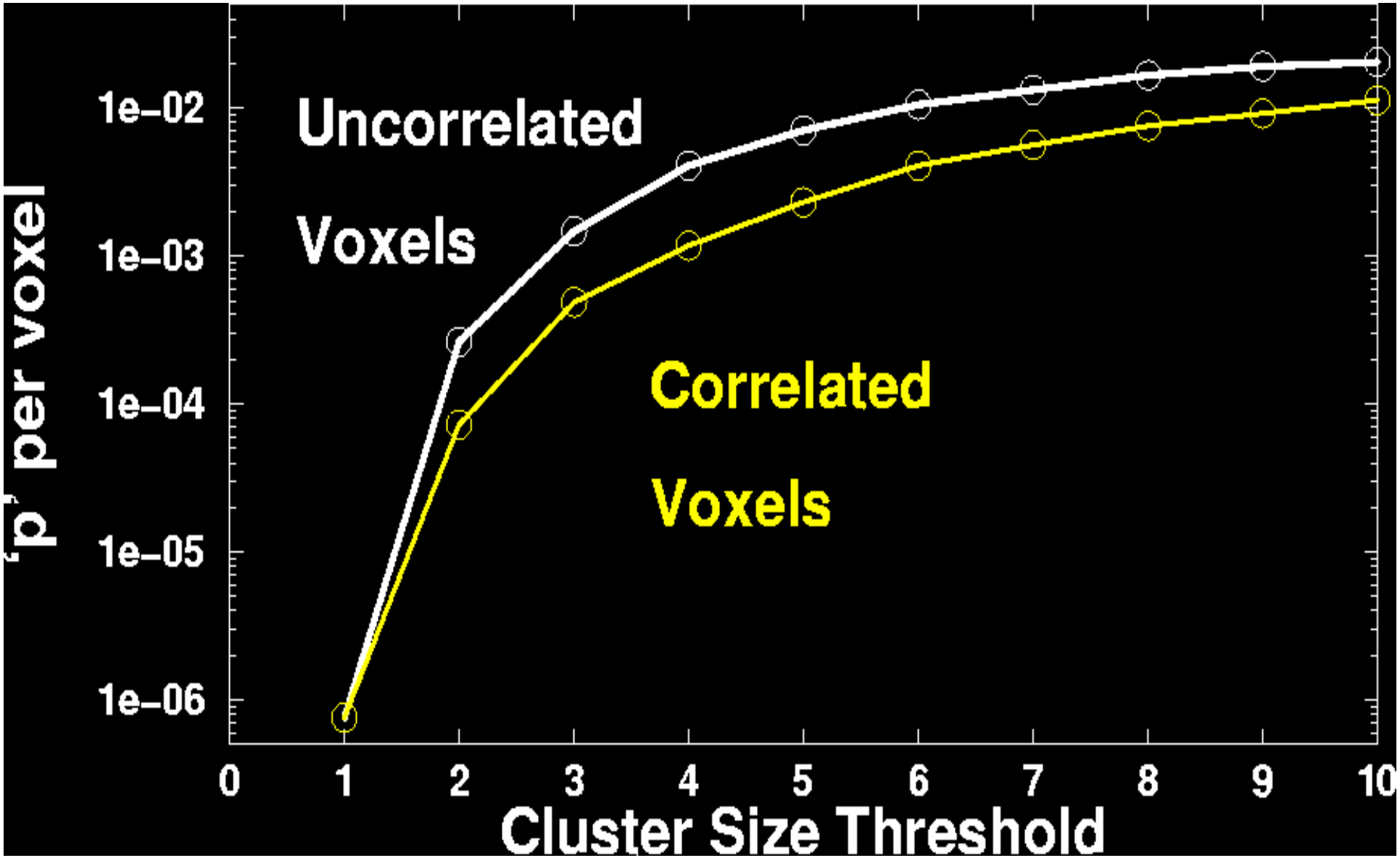
# Spatial Smoothing of Data

- Reduces number of comparisons
- Reduces noise (by averaging)
- Reduces spatial resolution
  - Blur it enough: Can make FMRI results look like low resolution PET data
- Smart smoothing: average ***only*** over nearby brain or gray matter voxels
  - Uses resolution of FMRI cleverly
    - New AFNI program: **`3dBlurToFWHM`**
  - Or: average over selected ROIs
  - Or: cortical surface based smoothing

# Spatial Clustering

- Analyze data, create statistical map (*e.g.*, ***t*** statistic in each voxel)
- Threshold map at a low ***t*** value, in each voxel separately
  - Will have many false positives
- Threshold map by rejecting clusters of voxels below a given size
- Can control false-positive rate by adjusting ***t*** threshold and cluster-size thresholds together

# Cluster-Based Detection



# What the World Needs Now

- Unified HRF/Deconvolution⊕Blob analysis
  - Time⊕Space patterns computed all at once, instead of arbitrary spatial smoothing
    - Increase statistical power by bringing data from multiple voxels together cleverly
  - Instead of time analysis followed by spatial analysis (described earlier)
  - Instead of component-style analyses (*e.g.*, ICA) that do not use stimulus timing

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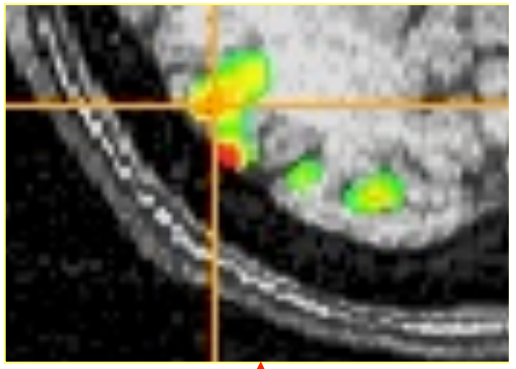
- Difficulty: models for spatial blobs
  - Little information *à priori* ⇒ must be adaptive

# 3dBlurToFWHM

- New program to smooth FMRI time series datasets to a specified smoothness (as estimated by FWHM of noise spatial correlation function)
  - ★ Don't just add smoothness (à la 3dmerge) but control it (locally and globally)
  - ★ Goal: use datasets from diverse scanners



- Why blur FMRI time series?
  - ★ Averaging neighbors will reduce noise
  - ★ Activations are (usually) blob-ish (several voxels across)
  - ★ Diminishes the multiple comparisons problem
- 3dBlurToFWHM blurs only inside a mask
  - ★ To avoid mixing air (noise-only) and brain voxels
  - ★ Partial Differential Equation (PDE) based blurring method
    - o 2D (intra-slice) or 3D blurring

# In the Pondering Stages

- "Area under curve" addition to `-gltsym` to allow testing of pieces of HRF models from `-stim_times`
- Slice- and/or voxel-dependent regressors
  - ★ For physiological noise cancellation, etc.
  - ★ To save memory? (Could process each slice separately)
    - o One slice-at-a-time regression can be done in a Unix script, using 3dZcutup and 3dZcat programs
- Extend AM regression to allow for more than 1 piece of auxiliary information at each stimulus time
- Interactive tool to examine `-x1D` matrix for problems
  - ★ and `3dDeconvolve` testing of GLT submatrices